

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/567,808  
Source: JFWO  
Date Processed by STIC: 02/16/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/567,808

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
    .  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length  
The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4      Non-ASCII  
The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length  
Sequence(s)          contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)          missing. If intentional, please insert the following lines for **each** skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)          missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>  
~~Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.~~  
~~Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.~~  
~~(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)~~
  
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa  
"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 02/16/2006

PATENT APPLICATION: US/10/567,808

TIME: 12:55:34

Input Set : A:\08321-0136PC.TXT

Output Set: N:\CRF4\02162006\J567808.raw

4 <110> APPLICANT: Thomas Jefferson University  
 5 Albert J. Wong  
 7 <120> TITLE OF INVENTION: METHOD FOR RAPID IDENTIFICATION OF  
 8 ALTERNATIVE SPLICING  
 10 <130> FILE REFERENCE: 08321-0136PC  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/567,808  
 C--> 12 <141> CURRENT FILING DATE: 2006-02-08  
 12 <150> PRIOR APPLICATION NUMBER: 60/493,759  
 13 <151> PRIOR FILING DATE: 2003-08-08  
 15 <160> NUMBER OF SEQ ID NOS: 3  
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 22  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Artificial Sequence  
 24 <220> FEATURE:  
 25 <223> OTHER INFORMATION: selectable tag  
 27 <400> SEQUENCE: 1  
 28 gtcattgcata gcaattgtcg ac  
 30 <210> SEQ ID NO: 2  
 31 <211> LENGTH: 17  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: Artificial Sequence  
 35 <220> FEATURE:  
 36 <223> OTHER INFORMATION: selectable tag  
 38 <400> SEQUENCE: 2  
 39 tcccccgggg ggaatcg  
 41 <210> SEQ ID NO: 3  
 42 <211> LENGTH: 27  
 43 <212> TYPE: DNA  
 44 <213> ORGANISM: Artificial Sequence  
 46 <220> FEATURE:  
 47 <223> OTHER INFORMATION: selectable tag  
 49 <400> SEQUENCE: 3  
 50 atgcatagca acctcacgtg tgaatcg  
 52 <210> SEQ ID NO: 4  
 53 <211> LENGTH: 21  
 54 <212> TYPE: DNA  
 55 <213> ORGANISM: Artificial Sequence  
 57 <220> FEATURE:  
 58 <223> OTHER INFORMATION: affinity medium  
 60 <400> SEQUENCE: 4  
 61 acacgtgagg ttgctatgca t

Does Not Comply  
Corrected Diskette Needed  
CPR-1,2)

Invalid Response.  
What is the Source of  
genetic material?  
Pls see Item # 11  
on Error Summary  
sheet

17

27

21

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/567,808

DATE: 02/16/2006

TIME: 12:55:34

Input Set : A:\08321-0136PC.TXT

Output Set: N:\CRF4\02162006\J567808.raw

63 &lt;210&gt; SEQ ID NO: 5

64 &lt;211&gt; LENGTH: 58

65 &lt;212&gt; TYPE: DNA

66 &lt;213&gt; ORGANISM: Artificial Sequence

68 &lt;220&gt; FEATURE:

69 &lt;223&gt; OTHER INFORMATION: polynucleotide linking moiety

71 &lt;400&gt; SEQUENCE: 5

72 acacgatccg cagatgtccg cagttattcc ttttttggaa taactgcgga catctgcg 58

74 &lt;210&gt; SEQ ID NO: 6

75 &lt;211&gt; LENGTH: 30

76 &lt;212&gt; TYPE: DNA

77 &lt;213&gt; ORGANISM: Artificial Sequence

79 &lt;220&gt; FEATURE:

80 &lt;223&gt; OTHER INFORMATION: arbitrary sequence

82 &lt;400&gt; SEQUENCE: 6

83 aaattcctat gcatgctcaa tggactgtgt

30

? Same error

? Same error

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/567,808

DATE: 02/16/2006

TIME: 12:55:35

Input Set : A:\08321-0136PC.TXT

Output Set: N:\CRF4\02162006\J567808.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date